OncoTree Documentation

Release 1.0

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CHAPTER

ONE

CONTENTS:

1.1 Python APIs created for this project

1.1.1 OncoTree module

OncoTree class

class OncoTree.OncoTree.**OncoTree**(*file_path=False*)

A OncoGxOne class to consume a tab delimited table of cancer type and construct tree structure class

Example

```
>>> from OncoTree import *
>>> OT = OncoTree
>>> print dir(OT)  # Check all methods applicable to OncoTree class
>>> ['OT', '__doc__', '__init__', '__module__', 'distance', 'homo', 'inclusion',
 ↪'url']
>>> print OT.url
>>> 'https://raw.githubusercontent.com/cBioPortal/oncotree/master/tumor_tree.txt'␣
 ↪ # This is default cancer type input
>>> print OT.abbrev['Leukemia']  # Check cancer type abbreviation. Note that the␣
 ↪dictionary key has to be exact match. Since the cancer type terminology is␣
 ↪mostly heterogeneous, please double check the cancer type metadata on url page␣
 ↪specified by OT.url
>>> 'LEUK'
>>> print OT.OT
>>> OT.OT # Return networkx clasee
>>> networkx.classes.digraph.DiGraph object at 0x21f0450>
>>> print OT.OT.successors('ALL')  # Check the successors of queried cancer type
>>> ['TALL', 'BALL']
>>> print OT.OT.predecessors('ALL') # Check the predecessors of queried cancer␣
 ↪type
>>> ['LEUK']
>>> print OT.inclusion('ALL')  # Check if input cancer type exist in OncoTree
>>> True
>>> print OT.homo('BALL', 'NSCLC')  # Check if two input cancer types are within␣
 ↪same lineage
>>> False
>>> print OT.distance('BALL', 'NSCLC')  # Calculate the distance between two␣
 ↪inpit cancer types
>>> 6
```

distance(*cop*, *coc*)

Function to calculate distance between two input cancer types

homo(*cop*, *coc*)
Function to check if two input cancer types in the same lineage

inclusion(*cop*)
Function to check if cancer type exist in oncotree

CHAPTER

TWO

UPDATES

2017-03-01:

- Add *abbrev* module to map full cancer type terminology to abrreviation

2017-02-24:

- The first version of OncoTree

CHAPTER

THREE

INDICES AND TABLES

- genindex
- modindex
- search

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